

S/N 09/804866

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method of analyzing argentinated peptides or argentinated proteins using mass spectrometry comprising: (a) combining an oligopeptide with silver to provide a sample comprising argentinated ~~argentated~~ oligopeptide; (b) submitting the sample to a mass spectrometer; (c) performing scans of silver containing peaks in optimum collision energies to maximize doublet or triplet peak patterns, wherein the scans are performed: (i) under increasing collision energies, identifying doublet and triplet peak patterns and determining the collision energies that maximize the doublet and/or triplet peak patterns, summing the spectra information from said optimum collision energies to produce a composite spectra that maximizes the doublet and/or triplet peak patterns; or (ii) over a range of collision energies to maximize the doublet and/or triplet peak patterns; (d) identifying any doublet or triplet peak pattern; (e) confirming with Y ions; and (f) determining partial sequence by the mass separation between two successive doublet or triplet patterns.
2. (currently amended) A method according to claim 1 wherein the performing scans comprises collecting product ion spectra of the $[M+Ag]^+$ ion, where M=oligopeptide, $[+]$
3. (currently amended) A method according to claim 1 wherein the oligopeptide consists of ~~comprises~~ from about 3 to about 10 amino acids.
4. (previously presented) A method according to claim 1 wherein the silver is silver nitrate.

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5. (currently amended) A method according to claim 1, wherein the step of determining determination of partial sequence by the mass separation between two successive doublet or triplet patterns further comprises searching for, and identifying cleaved amino acid residues based on differences in m/z values of neighboring triplets where the m/z value of the $[b_n - H + Ag]^+$ ion and the corresponding $[y_n + H + Ag]^+$ ion are related by the formula: $[y_n + H + Ag]^+ = [M + Ag]^+ + Ag^+ - [b_n - H + Ag]^+$.
6. (original) A method according to claim 5 wherein the searching and identifying is conducted by a custom search algorithm.
7. (currently amended) A method according to claim 6 wherein the algorithm is written in Visual Basic and identifies both ~~looks for~~ the triplet peak pattern of $(m/z)_1$, $(m/z)_2 = (m/z)_1 - 18.0$, and $(m/z)_3 = (m/z)_2 - 28.0$ as well as the doublet pattern of $(m/z)_2$ and $(m/z)_3$, all to within ± 0.5 m/z unit.
8. (currently amended) A method according to claim 2 wherein product ion spectra of the $[M + Ag]^+$ ion are collected under E_{cm} s, of 1.5, 2.0, 2.5 and 3.0 eV.
9. (previously presented) A method according to claim 1 wherein the mass spectrometer is a triple quadrupole mass spectrometer, two triple quadrupole mass spectrometers, a quadrupole/time-of-flight mass spectrometer, an ion-trap mass spectrometer, or a time-of-flight mass spectrometer amenable to post-source decay or collision-induced dissociation.
10. (currently amended) A method of analyzing argenitinated peptides or argenitinated proteins using mass spectrometry comprising: (a) combining an oligopeptide with silver nitrate in solution; (b) submitting a sample of the solution to a mass spectrometer; (c) collecting product ion spectra of the $[M + Ag]^+$ ion, where M=oligopeptide; (d) identifying a triplet peak pattern; (e) identifying a doublet peak pattern; and (f) searching for, and identifying cleaved amino acid residues based on differences in m/z values of neighboring triplets where the m/z value of the

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$[b_n-H+Ag]^+$ ion and the corresponding $[y_n+H+Ag]^+$ ion are related by the formula:

$$[y_n+H+Ag]^+ = [M+Ag]^+ + Ag^+ - [b_n-H+Ag]^+$$

11. (currently amended) A method according to claim 10 wherein the oligopeptide consists of ~~comprises~~ from about 3 to about 10 amino acids.

12. (previously presented) A method according to claim 10 wherein the searching and identifying is conducted by a custom search algorithm.

13. (original) A method according to claim 12 wherein the algorithm is written in Visual Basic and looks for the triplet peak pattern of $(m/z)_1$, $(m/z)_2 = (m/z)_1 - 18.0$, and $(m/z)_3 = (m/z)_2 - 28.0$ as well as the doublet pattern of $(m/z)_2$ and $(m/z)_3$, all to within ± 0.5 m/z unit.

14. (previously presented) A method according to claim 10 wherein product ion spectra of the $[M + Ag]^+$ ion are collected under $E_{cm,s}$, of 1.5, 2.0, 2.5 and 3.0 eV.

15. (previously presented) A method according to claim 10 wherein the mass spectrometer is a triple quadrupole mass spectrometer, two triple quadrupole mass spectrometers, a quadrupole/time-of-flight mass spectrometer, an ion-trap mass spectrometer, or a time-of-flight mass spectrometer amenable to post-source decay or collision-induced dissociation.